

Copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6	30	17	68.0	823	2	T02812
OM protein - protein search, using sw model	31	17	68.0	870	2	AB0570	
Run on: January 31, 2005, 18:10:30 i	Search time 20 Seconds (without alignments)	32	17	68.0	1029	2	F96602
Title: US-10-083-768-5	48.108 Million cell updates/sec	33	17	68.0	1156	2	S19306
Perfect score: 25	GP340 protein prec	34	17	68.0	1275	1	S53636
Sequence: 1 XXGXXXXWX 10	Ribulose-bisphosphate carboxylase	35	17	68.0	1546	2	G90603
Scoring table: BLOSUM62	hypothetical protein	36	17	68.0	1596	2	AG2501
Gapop 10.0 , Gapext 0.5	hypothetical protein	37	17	68.0	1680	1	C5MS
Searched: 283416 seqs, 96216763 residues	probable membrane protein	38	17	68.0	2062	2	G96602
Total number of hits satisfying chosen parameters: 283416	outer membrane usher protein	39	17	68.0	2204	1	RRN27V
Minimum DB seq length: 0	polioprotein B-1	40	17	68.0	4563	1	LPHUB
Maximum DB seq length: 2000000000	hypothetical protein	41	17	68.0	4660	2	T42737
Post-processing: Minimum Match 0%	GP340 protein prec	42	16	64.0	12	PQ0776	
Maximum Match 100%	NADH2 dehydrogenase	43	16	64.0	60	AC29981	
Listing First 45 summaries	hypothetical protein	44	16	64.0	66	T35419	
Database : PIR_79;*	small hypothetical protein	45	16	64.0	70	A30518	
1: Piri1;*	Ig heavy chain V-A						
2: Piri2;*							
3: Piri3;*							
4: Piri4;*							
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	Description		
-	-	-	-	-	hypothetical protein		
1	17	68.0	72	H90603	hypothetical protein		
2	17	68.0	132	2	hypothetical 14.2K		
3	17	68.0	165	2	hypothetical 14.2K		
4	17	68.0	203	2	hypothetical protein		
5	17	68.0	239	2	superoxide dismutase		
6	17	68.0	251	2	hypothetical protein		
7	17	68.0	272	2	NADH-Flavin Oxido		
8	17	68.0	297	2	hypothetical protein		
9	17	68.0	308	2	probable sugar uptake protein		
10	17	68.0	406	2	hypothetical protein		
11	17	68.0	408	2	hypothetical protein		
12	17	68.0	408	2	probable FAD-linker		
13	17	68.0	433	2	hypothetical protein		
14	17	68.0	492	2	hemolysin - Aeromonas		
15	17	68.0	523	2	probable secreted protein		
16	17	68.0	547	2	hypothetical protein		
17	17	68.0	579	2	probable secreted protein		
18	17	68.0	624	2	alpha-galactosidase		
19	17	68.0	735	2	conserved hypothetical protein		
20	17	68.0	776	1	outer layer protein		
21	17	68.0	776	1	outer layer protein		
22	17	68.0	776	1	outer layer protein		
23	17	68.0	776	1	outer layer protein		
24	17	68.0	776	1	outer layer protein		
25	17	68.0	776	1	outer layer protein		
26	17	68.0	776	1	outer layer protein		
27	17	68.0	776	1	outer layer protein		
28	17	68.0	776	2	outer capsid protein		
29	17	68.0	776	2	outer layer protein		
ALIGNMENTS							
RESULT 1							
H90603							
hypothetical protein MYPU_7360 [imported] - Mycoplasma pulmonis (strain UAB CTIP)							
C;Species: Mycoplasma pulmonis							
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004							
C;Accession: H90603							
R;Chambard, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Gallisson, F.; Moszer, I.; Nucleic Acids Res, 29, 2145-2153, 2001							
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis							
A;Reference number: A99312; MUID:21267165; PMID:113531084							
A;Accession: H90603							
A;Status: Preliminary							
A;Molecule type: DNA							
A;Residues: 1-72 <KUR>							
A;Cross-references: UNIPROT:Q98PI6; GB:AL445566; PID:914090151; PIDN:CAC13909_1; GSPDB:G							
A;Experimental source: strain UAB CTIP							
C;Genetics:							
A;Gene: MYPU_7360							
A;Genetic code: SCG3							
RESULT 2							
Query Match	68.0%	Score 17;	DB 2;	Length 72;			
Best Local Similarity	28.6%	Pred. No.	8.6e+02;				
Matches 2;	Conservative	0;	Mismatches 5;				
Indels 0;	Gaps 0;						
QY	3 GXXXXXW 9						
Db	39 GAATSW 45						
RESULT 2							
C41855							
hypothetical 14.2K beta-lactamase regulatory protein - Streptomyces cacaoi							
C;Species: Streptomyces cacaoi							
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004							
C;Accession: C41855							
R;Drabe, H.; Ogawara, H.							
J. Bacteriol. 174, 2834-2842, 1992							
A;Title: Nucleotide sequence and transcriptional analysis of activator-regulator protein A;Reference number: A11855; MUID:92234939; PMID:1569015							
A;Accession: C41855							
A;Status: Preliminary							
A;Molecule type: DNA							
A;Residues: 1-132 <URA>							
A;Cross-references: UNIPROT:P33554; GB:D00937; PID:9216997; PIDN:BA00776_1; PID:9217001							
A;Note: Sequence extracted from NCBI backbone (NCBIN:97018, NCBIPI:97029)							
C;Superfamily: Streptomyces cacaoi hypothetical 14.2K beta-lactamase regulatory protein							
Query Match	68.0%	Score 17;	DB 2;	Length 132;			
Best Local Similarity	28.6%	Pred. No.	1.4e+03;				
Matches 2;	Conservative	0;	Mismatches 5;				
Indels 0;	Gaps 0;						
QY	3 GXXXXXW 9						

Db 53 GSSASSW 59

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-239 <SEE>

A;Cross-references: UNIPROT:Q9S1Z1; EMBL:AU109747; PIDN:CAE52362.1; GSPDB:GN00070; SCOED1

A;Experimental source: strain A3 (2)

C;Genetics: SCOEDB:SCU21.16

C;Species: *Pseudomonas aeruginosa*

C;ID: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: A83349

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bradian, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic pathogen

A;Reference number: A82349

A;Accession: A83349

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-165 <STO>

A;Cross-references: UNIPROT:Q911B2; GB:AE004663; GB:AE004091; PIDN:ANG0575

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA2267

Query Match 68.0%; Score 17; DB 2; Length 165;

Best Local Similarity 28.6%; Pred. No. 2.3e+03; Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirano, T.; Nakagawa, H.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its genome comparison with *Bacillus subtilis*

A;Reference number: A82650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; PIDN:910175500; PIDN:BAE000004; PIDN:910175500; PIDN:BAE0666;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2953

C;Superfamily: NADPH-Flavin oxidoreductase homolog

Query Match 68.0%; Score 17; DB 2; Length 251;

Best Local Similarity 28.6%; Pred. No. 2.4e+03; Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirano, T.; Nakagawa, H.

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A;Reference number: A82650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; PIDN:910175500; PIDN:BAE000004; PIDN:910175500; PIDN:BAE0666;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2953

C;Superfamily: NADPH-Flavin oxidoreductase homolog

Query Match 68.0%; Score 17; DB 2; Length 251;

Best Local Similarity 28.6%; Pred. No. 2.4e+03; Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirano, T.; Nakagawa, H.

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A;Reference number: A82650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; PIDN:910175500; PIDN:BAE000004; PIDN:910175500; PIDN:BAE0666;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2953

C;Superfamily: NADPH-Flavin oxidoreductase homolog

Query Match 68.0%; Score 17; DB 2; Length 251;

Best Local Similarity 28.6%; Pred. No. 2.4e+03; Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirano, T.; Nakagawa, H.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its genome comparison with *Bacillus subtilis*

A;Reference number: A82650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; PIDN:910175500; PIDN:BAE000004; PIDN:910175500; PIDN:BAE0666;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2953

C;Superfamily: NADPH-Flavin oxidoreductase homolog

Query Match 68.0%; Score 17; DB 2; Length 251;

Best Local Similarity 28.6%; Pred. No. 2.4e+03; Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirano, T.; Nakagawa, H.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its genome comparison with *Bacillus subtilis*

A;Reference number: A82650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; PIDN:910175500; PIDN:BAE000004; PIDN:910175500; PIDN:BAE0666;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2953

C;Superfamily: NADPH-Flavin oxidoreductase homolog

Query Match 68.0%; Score 17; DB 2; Length 251;

Best Local Similarity 28.6%; Pred. No. 2.4e+03; Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirano, T.; Nakagawa, H.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its genome comparison with *Bacillus subtilis*

A;Reference number: A82650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; PIDN:910175500; PIDN:BAE000004; PIDN:910175500; PIDN:BAE0666;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2953

C;Superfamily: NADPH-Flavin oxidoreductase homolog

Query Match 68.0%; Score 17; DB 2; Length 251;

Best Local Similarity 28.6%; Pred. No. 2.4e+03; Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirano, T.; Nakagawa, H.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its genome comparison with *Bacillus subtilis*

A;Reference number: A82650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; PIDN:910175500; PIDN:BAE000004; PIDN:910175500; PIDN:BAE0666;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2953

C;Superfamily: NADPH-Flavin oxidoreductase homolog

Query Match 68.0%; Score 17; DB 2; Length 251;

Best Local Similarity 28.6%; Pred. No. 2.4e+03; Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirano, T.; Nakagawa, H.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its genome comparison with *Bacillus subtilis*

A;Reference number: A82650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; PIDN:910175500; PIDN:BAE000004; PIDN:910175500; PIDN:BAE0666;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2953

C;Superfamily: NADPH-Flavin oxidoreductase homolog

Query Match 68.0%; Score 17; DB 2; Length 251;

Best Local Similarity 28.6%; Pred. No. 2.4e+03; Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirano, T.; Nakagawa, H.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its genome comparison with *Bacillus subtilis*

A;Reference number: A82650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; PIDN:910175500; PIDN:BAE000004; PIDN:910175500; PIDN:BAE0666;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2953

C;Superfamily: NADPH-Flavin oxidoreductase homolog

Query Match 68.0%; Score 17; DB 2; Length 251;

Best Local Similarity 28.6%; Pred. No. 2.4e+03; Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirano, T.; Nakagawa, H.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its genome comparison with *Bacillus subtilis*

A;Reference number: A82650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; PIDN:910175500; PIDN:BAE000004; PIDN:910175500; PIDN:BAE0666;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2953

C;Superfamily: NADPH-Flavin oxidoreductase homolog

Query Match 68.0%; Score 17; DB 2; Length 251;

Best Local Similarity 28.6%; Pred. No. 2.4e+03; Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirano, T.; Nakagawa, H.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its genome comparison with *Bacillus subtilis*

A;Reference number: A82650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; PIDN:910175500; PIDN:BAE000004; PIDN:910175500; PIDN:BAE0666;

A;Experimental source: strain C-125

C;Genetics:

A;Gene: BH2953

C;Superfamily: NADPH-Flavin oxidoreductase homolog

Query Match 68.0%; Score 17; DB 2; Length 251;

Best Local Similarity 28.6%; Pred. No. 2.4e+03; Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

C;Accession: A84019

R;Pakami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Fuji, F.; Hirano, T.; Nakagawa, H.

Nucleic Acids Res. 28, 4317-4331, 2000

A;Title: Complete genome sequence of the alkaliiphilic bacterium *Bacillus halodurans* and its genome comparison with *Bacillus subtilis*

A;Reference number: A82650; PMID:11058132

A;Accession: A84019

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-251 <STO>

A;Cross-references: UNIPROT:Q9K8Q0; GB:AP001517; PIDN:910175500; PIDN:BAE000004; PIDN:910175500; PIDN:BAE0666;

A;Experimental source: strain C-125</

RESULT 8
 E96002 probable sugar uptake ABC transporter permease protein SMB21459 [imported] - Sinorhizobi
 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C;Accession: E96002
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buijrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
 A;Reference number: A95842; MUID:21396508; PMID:11481431
 A;Accession: E96002
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-257 <KUR>
 A;Cross-references: UNIPROT:Q92U54; GB:AL591985; PIDN: CAC49685.1; PID:915141172; GSPPDB:G
 A;Experimental source: strain 1021, megaplasmid pSymB
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 Peila, D.; Chain, P.; Cowie, A.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 658-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Kopp, C.; Lelaurie,
 heault, P.; Vandembol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A;Content: number: A95842; MUID:21396508; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: SMB21459
 A;Genome: Plasmid
 C;Superfamily: inner membrane protein uGPA

Query Match 68.0%; Score 17; DB 2; Length 297;
 Best Local Similarity 28.6%; Pred. No. 2.7e+03; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 5; Indels 5; Gaps 0;

Qy 3 GXXXXW 9
 Db 268 GAAASTW 274

RESULT 9
 B84311 hypothetical protein Vng1578h [imported] - Halobacterium sp. NRC-1
 C;Species: Halobacterium sp. NRC-1
 C;Accession: B84311
 R;ING, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.
 Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablon
 Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
 A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebbhardt, H.; Lowe, T.M.; Li
 A;Title: Genome sequence of Halobacterium species NRC-1.
 A;Reference number: A84160; MUID:20504483; PMID:11016950
 A;Accession: B84311
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-308 <SNO>
 A;Cross-references: UNIPROT:Q9HPL3; GB:AB004437; NID:910581062; PIDN:AAG19854.1; GSPPDB:G
 C;Genetics:
 A;Gene: VNG1578H
 C;Superfamily: cobalamin biosynthesis protein D

Query Match 68.0%; Score 17; DB 2; Length 308;
 Best Local Similarity 28.6%; Pred. No. 2.8e+03; Indels 0; Mismatches 5; Indels 5; Gaps 0;

Qy 3 GXXXXW 9
 Db 172 GAAAAAW 178

RESULT 8
 A47696 acetamidase - Mycobacterium smegmatis
 C;Species: Mycobacterium smegmatis
 C;Accession: A47696
 R;Mahenthiralingam, E.; Draper, P.; Davis, E.O.; Colston, M.J.
 J. Gen. Microbiol. 139, 575-583, 1993
 A;Title: Cloning and sequencing of the gene which encodes the highly inducible acetamida
 A;Reference number: A47696; MUID:9323274; PMID:1473853
 A;Contents: NCTC 8159
 A;Accession: A47696
 A;Status: preliminary
 A;Molecule type: DNA; protein
 A;Residues: 1-406 <MAH>
 A;Cross-references: UNIPROT:007838; GB:X57175; PIDN:G312080; PIDN:CA440462.1;
 A;Note: sequence inconsistent with the nucleotide translation on NCBI backbone (NCBIN129965, NCBIPI:129966)
 A;Note: sequence extracted from NCBI backbone (NCBIN129965, NCBIPI:129966)
 Query Match 68.0%; Score 17; DB 2; Length 406;
 Best Local Similarity 28.6%; Pred. No. 3.5e+03; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 5; Indels 5; Gaps 0;
 Qy 3 GXXXXW 9
 Db 370 GASASW 376

RESULT 11
 D70549 hypothetical protein Rv0561c - Mycobacterium tuberculosis (strain H37RV)
 C;Species: Mycobacterium tuberculosis
 C;Accession: D70549
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, C.; Churcher, C.; Gordon, D.; Gordon, S.; Connors, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.; Nature 393, 537-544, 1998
 A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.; A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A;Content: number: A70500; MUID:98295587; PMID:9634230
 A;Accession: D70549
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-408 <COL>
 A;Cross-references: UNIPROT:006427; GB:295558; PIDN:CA08972.
 A;Experimental source: strain H37RV
 C;Genetics:
 A;Gene: Rv0561c
 C;Superfamily: fixC protein

Query Match 68.0%; Score 17; DB 2; Length 408;
 Best Local Similarity 28.6%; Pred. No. 3.5e+03; Indels 0; Mismatches 5; Indels 0; Gaps 0;

Qy 3 GXXXXW 9
 Db 18 GAAAAW 24

RESULT 12
 H87193 probable PAD-linked oxidoreductase ML2276 [imported] - Mycobacterium leprae
 C;Species: Mycobacterium leprae
 C;Accession: H87193
 R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; Ho
 R.; Davies, R.M.; Devlin, K.; Dutchoy, S.; Feltwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
 M.A.; Rutherford, K.M.; Nature 409, 1007-1011, 2001
 A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
 A;Reference number: A86509; MUID:21128732; PMID:11234002
 A;Accession: H87193

A;Status: preliminary	Qy	3	GXXXXW	9	Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
A;Molecule type: DNA	Db	91	GSATTW	97	
A;Residues: 1-409 <STO>					
A;Cross-references: UNIPROT:Q9CBA6; GB:AL450380; NID:913093912; PIDN:CAAC31792.1; GSPDB:Q					
C;Generics:					
A;Gene: ML2276					
Query Match 68.0%; Score 17; DB 2; Length 408;					RESULT 15
Best Local Similarity 28.6%; Pred. No. 3.5e+03;					T36677
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;					probable secretory protein - <i>Streptomyces coelicolor</i>
Qy 3 GXXXXW 9					C;Species: <i>Streptomyces coelicolor</i>
Db 18 GSAAATW 24					C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
					C;Accession: T36677
					R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Barrell, B.G.; Rajandream, M.A.
					A;Submitted to the EMBL Data Library, March 1999
					A;Reference number: Z21611
					A;Accession: T36677
					A;Status: preliminary; translated from GB/EMBL/DBJ
					A;Molecule type: DNA
					A;Residues: 1-523 <SEE>
					A;Cross-references: UNIPROT:Q9X921; EMBL:AU035636; PIDN:CAAB38493.1; GSPDB:GN00070; SCOED1
					A;Experimental source: strain A3(2)
					C;Genetics:
					Query Match 68.0%; Score 17; DB 2; Length 523;
					Best Local Similarity 28.6%; Pred. No. 4.3e+03;
					Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
					Qy 3 GXXXXW 9
					Db 85 GSATTW 91
					Search completed: January 31, 2005, 18:22:34
					Job time : 21 secs
RESULT 13					
C69222					
hypothetical protein MTH913 - <i>Methanobacterium thermoautotrophicum</i> (strain Delta H)					
C;Species: <i>Methanobacterium thermoautotrophicum</i>					
C;Accession: C69222					
C;Title: 05-Dec-1997 #Sequence_revision 05-Dec-1997 #text_change 09-Jul-2004					
R;Smith, D.R.; Doucette-Stamm, L.A.; Delouhery, C.; Lee, H.; Dubois, J.; Aldredge, T.J.					
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.					
; Ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.					
J. Bacteriol. 179, 7135-7155, 1997					
J. Title: Complete genome sequence of <i>Methanobacterium thermoautotrophicum</i> Delta H: funct					
A;Reference number: A69000; PMID:98037514; PMID:9371463					
A;Status: preliminary; nucleic acid sequence not shown; translation not shown					
A;Molecule type: DNA					
A;Cross-references: UNIPROT:O26998; GB:AE000666; NID:92622009; PIDN:MRB8541					
A;Experimental source: strain Delta H					
C;Genetics:					
A;Gene: MTH913					
A;Start codon: GTG					
Query Match 68.0%; Score 17; DB 2; Length 433;					
Best Local Similarity 28.6%; Pred. No. 3.7e+03;					
Matches 2; Conservative 0; Mismatches 5; Indels 0; Gaps 0;					
Qy 3 GXXXXW 9					
Db 391 GSATSSW 397					
RESULT 14					
I39591					
hemolysin - <i>Aeromonas hydrophila</i>					
N;Alternate names: aerolysin					
C;Species: <i>Aeromonas hydrophila</i>					
C;Accession: I39591; I39590; S26573; S2574					
R;Hirano, I.; Aoki, T.; Asao, T.; Kozaki, S.					
Microb. Pathog. 13, 433-446, 1992					
A;Title: Nucleotide sequences and characterization of haemolysin genes from <i>Aeromonas</i> hy					
A;Reference number: I39590; PMID:93254202; PMID:1302284					
A;Status: preliminary; translated from GB/EMBL/DBJ					
A;Molecule type: DNA					
A;Residues: 1-492 <RES>					
A;Cross-references: UNIPROT:Q06303; EMBL:X65043; NID:938816; PIDN:CAA46179.1; PID:938817					
A;Accession: I39590					
A;Status: preliminary; translated from GB/EMBL/DBJ					
A;Molecule type: DNA					
A;Residues: 1-56, 'V' 58-295, 'P' 297-492 <RES>					
A;Cross-references: EMBL:K65044; NID:938814; PIDN:CAA46180.1; PID:938815					
A;Experimental source: strain 28SA					
C;Superfamily: aerolysin					
Query Match 68.0%; Score 17; DB 2; Length 492;					
Best Local Similarity 28.6%; Pred. No. 4.1e+03;					